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         5      10      15      20      25      30      35      40      45
        ATG GGT GCA GGT GCA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT
        TAC CCA CGT CCA CCT TCT TAC GTT CAC AGA GGA GGG ACG TTT TTC AGA
         M   G   A   G   A   R   M   Q   V   S   P   P   S   K   K   S>

         50      55      60      65      70      75      80      85      90      95
        GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT
        CTT TGG CTG TTG TAG TTC GCG CAT GGG ACG CTC TGT GGC GGG AAG TGA
         E   T   D   N   I   K   R   V   P   C   E   T   P   P   F   T>

        100     105     110     115     120     125     130     135     140
        GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG
        CAG CCT CTT GAG TTC TTT CGT TAG GGT GGC GTG ACA AAG TTT GCG AGC
         V   G   E   L   K   K   A   I   P   P   H   C   F   K   R   S>

        145     150     155     160     165     170     175     180     185     190
        ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATA GCC TCC
        TAG GGA GCG AGA AAG AGG ATG GAG TAG ACC CTG TAG TAT CGG AGG
         I   P   R   S   F   S   Y   L   I   W   D   I   I   A   S>

        195     200     205     210     215     220     225     230     235     240
        TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT
        ACG AAG ATG ATG CAG CGG TGG TGA ATG AAG GGA GAG GAG GGA GTG GGA
         C   F   Y   Y   V   A   T   T   Y   F   P   L   L   P   H   P>

        245     250     255     260     265     270     275     280     285
        CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TCC CAG GGC TGC GTC
        GAG AGG ATG AAG CGG ACC GGA GAG ATG ACC CGG AGG GTC CCG ACG CAG
         L   S   Y   F   A   W   P   L   Y   W   A   C

        290     295     300     305     310     315     320     325     330     335
                                        A (K)          →
        CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC CAC GCC TTC
        GAT TGG CCG CAG ACC CAG TAT CGG GTG CTC ACG CCG GTG GTG CGG AAG

        340     345     350     355     360     365     370     375     380
        AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC TTC CAC TCC
        TCG CTG ATG GTC ACC GAC CTG TGG CAG CCG GAG TAG AAG GTG AGG
                                         D   T   V   G   L   I   F   H   S>

        385     390     395     400     405     410     415     420     425     430
        TTC CTC CTC GTC CCT TAC TTC TCC TGC AAG TAC AGT CAT CGA CGC CAC
        AAG GAG GAG CAG GGA ATG AAG AGG ACC TTC ATG TCA GTA GCT GCG GTG
         F   L   L   V   P   Y   F   S   M   K   Y   S   H   R   R   H>

        435     440     445     450     455     460     465     470     475     480
        CAT TCC AAC ACT GGC TCC CTC GAG ACA GAC GAA GTG TTT GTC CCC AAG
        GTA AGG TTG TGA CCG AGG GAG CTC TCT CTG CTT CAC AAA CAG GGG TTC
         H   S   N   T   G   S   L   E   R   D   E   V   F   V   P   R>

        485     490     495     500     505     510     515     520     525
        AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG
        TTC TTC AGT CTG TAG TTC ACC ATG CCG TTC ATG GAG TTG TTG GGA AAC
         K   K   S   D   I   K   W   Y   G   K   Y   L   N   N   P   L>

        530     535     540     545     550     555     560     565     570     575
        GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG
        CCT GCG TGG CAC TAC AAT TGC CAA GTC AAG TGA GAG CCG ACC GGA AAC
         G   R   T   V   M   L   T   V   Q   F   T   L   G   W   P   L>

        580     585     590     595     600     605     610     615     620
        TAC TTA GCC TTC AAC GTC TGG GGG AGA CCT TAC GAC GGC GGC TTC GCT
        ATG AAT CGG AAG TTG CAG ACC CCC TCT GGA ATG CTG CCG CCG AAG CGA
         Y   L   A   F   N   V   W   G   R   P   Y   D   G   G   F   A>
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Right margin handwritten notes:

DNA and deduced protein sequence from vector FAD2 (B) clone.

In 129 and Q508 clones (E) GAG was converted to AAG (K). This mutation was found in F clone only.

BP but occur in both 129 and Q508 mutant lines.

Again, this region was confirmed from

RIMENTER _(signature)_   DATE ▮▮▮
ISSUED BY _(signature)_   DATE ▮▮▮

TITLE ___ cont'd ___ DATE ___ Page No. __ 143

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        625    630    635    640    645    650    655    660    665    470
        TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CCT CTC
        ACG GTA AAG GTG GGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG
         C   H   F   H   P   N   A   P   I   Y   N   D   R   E   L>

        675    680    685    690    695    700    705    710    715    720
        CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC
        GTC TAT ATG TAG AGG CTG CGA CCG TAG GAG CGG CAG ACG ATG CCA GAG
         Q   I   Y   I   S   D   A   G   I   L   A   V   C   Y   G   L>

              725    730    735    740    745    750    755    760    765
        TAC CGC TAC GCT GCT GTC CAA GGA GTT GCC TCG ATG GTC TGC TTC TAC
        ATG GCG ATG CGA CGA CAG GTT CCT CAA CGG AGC TAC CAG ACG AAG ATG
         Y   R   Y   A   A   V   Q   G   V   A   S   M   V   C   F   Y>

        770    775    780    785    790    795    800    805    810    815
        GGA GTT CCG CTT CCG ATT GTC AAT GGG TTC TTA GTT TTG ATC ACT TAC
        CCT CAA GGC GAA GGC TAA CAG TTA CCC AAG AAT CAA AAC TAG TGA ATG
         G   V   P   L   L   I   V   N   G   F   L   V   L   I   T   Y>

         820    925    930    835    845    845    850    855    860
        TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG TCT GAG TGG
        AAC GTC GTG TGC GTA GGA AGG GAC GGA GTC ATA CTG AGC AGA CTC ACC
         L   Q   H   T   H   P   S   L   P   H   Y   D   S   S   E   W>

        865    870    875    880    885    890    895    900    905    910
        CAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC ACA GAC TAC GGA ATC
        GTA ACC AAC TCC CCT CGA AAC CGG TGG CAA CTG TCT CTG ATG CCT TAG
         D   W   L   R   G   A   L   A   T   V   D   R   D   Y   G   I>

        915    920    925    930    935    940    945    950    955    960
        TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG GCG CAT CAC
        AAC TTG TTC CAG AAG GTG TTA TAG TGC CTG TGC GTG CAC CGC GTA GTG
         L   N   K   V   F   H   N   I   T   D   T   H   V   A   H   H>

        965    970    975    980    985    990    995    1000   1005
        CTG TTC TCG ACC ATG CCG CAT TAT CAT CCG ATC GAA GCT ACG AAG CCG
        GAC AAG AGC TGG TAC GGC GTA ATA GTA CGC TAG CTT CGA TGC TTC GGC
         L   F   S   T   M   P   H   Y   H   A   M   E   A   T   K   A>

        1010   1015   1020   1025   1030   1035   1040   1045  1050  1055
        ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTG CAT GGG ACG CCG GTC
        TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAC GTA CCC TGC GGC CAC
         I   K   P   I   L   G   E   Y   Y   Q   L   H   G   T   P   V>

        1060   1065   1070   1075   1080   1085   1090   1095   1100
        GTT AAG GCG ATG TGG AGG CAG GCG AAG GAG TGT ATC TAT CTG GAA CCG
        CAA TTC CGC TAC ACC TCC GTC CGC TTC CTC ACA TAG ATA CAC CTT GGC
         V   K   A   M   W   R   E   A   K   E   C   I   Y   V   E   P>

        1105   1110   1115   1120   1125   1130   1135   1140   1145  1150
        GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA
        CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT
         D   R   Q   G   E   K   K   G   V   F   W   Y   N   N   K   L>

        1155   1160   1165   1170
        TGA AGC AAA GAA GAA ACA AT
        ACT TCG TTT CTT CTT TGT TA
          *   S   K   E   E   T   X>
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(handwritten right column)

with strands

(see page 134)

for primer location

Total 5 independent 123 and 0508 clones (each with 0in) were sequenced by primer DR (see page 134) and showed the same mutation.

Thus it appears to be true mutation.

This will be further confirmed by RT-PCR RNA from 123 infected and expressed by DR primer